



- SEG IDNO: 2 A-SEG ID NO: 1 D-SEG ID NO: 2

SEG 10 NO: 3 四日

SEG ID NO. 4 11

ING2:	\ AAAGCGTTCTCGGCGGCAGCAACAACTAGAACCGTGAGAACGCGTCCAGCAACCGCGACCCACGACGACGTCA	75
ING1 (D):	C \CA	
ING2:	CCTCGGGCACGCCCAAGGAGAAAGCCCAGACCTCTAAGAAGAAGCAGGGCTCCATGGCCAAGGCGTAGCGGC	150
ING1 (D):	\.A	
ING2:	AGGCGTCCCCGCAGACCTCCCCATCGACCCCAGCGAGCCCTCCTACTGG	201
ING1 (D):	\TCAAGTCTGTGCAACCAGGTCTCCTATGGG.	
ING2:	AGATGATCCGCTGCGACAACGAATGCCCCATCGAGTGGTTCCGCTTCTCGTGTGTGAGTCTCAACCATAAAC	273
ING1 (D):		
ING2:	<u>CAAAGCGCAAGTGGTACTGTTCCAGAGGCCGGGGAAAGAACGATGGGCAAAGCCCTTGA</u> GAAGTCCA	340
ING1 (D):	.CGCAGGGGAAGACCAA	
ING2:	GAAAAAAACAGGCTTATAACAGCTAGTTTGGGGACATGCGTCTAATAGTGAGGAGAACAAAATAAGCCAGTGT	415
ING1 (D):	G.G\dot\dot\dot\dot\dot\dot\dot\dot\dot\dot	
ING2:	GTTGATTACATTGCCACCTTTGCTGAGGTGCAGGAAGTGTAAAATGTATATTTTTAAAGAATGTTGTTAGAGGCC	490
ING1 (D):	ATAGA.AAA	
ING2:	GGGCGCGGTGGCTCACGÒCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGTCGGATCACGAGGTCAGGAGATCG	565
ING1 (D):	CCATT.CT.TCA.AGG.A.\Gd.GTGATT.TGCCTTTTGTTTT.AT.G.TT.TAACAAGA.AGT	
ING2:	AGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATTCAAAAAAAA	640
ING1 (D):	G.T.TG.GGATCAGC.TTTTATA.AAA.AGGTTTGC.CTTG.CTCAGACTGA.TTCTTG	
ING2:	GGGCGCCTGTAGTCCCAGCTATTCGGGAGGCTGAGGCAGGAGAATGGCNTGAACCTGGGAGGTGGAGCTTGCANT	715
ING1 (D):	CGAGGAGGG.GA.T.AACTCA.CCT.ACACATTAA.TGT.G.AAAAAT.TTTCATTA.CTTTTT.ATTTTA	
ING2:	GAGCCAAGGTCGCGCCACTGCACTCQAGCCTGGGCGACAGAGCGAGACTCCATCTTA	772
ING1 (D):	ATATAATATTACTTTATG\A.AATTTTTTTA.TT.GCCA.GTCG.CA.	

ING2 = SEQ 10 NO: 8 ING1(D) = SEQ 10 NO: 2 (part)

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SEGIDNO. 15

 $\texttt{CTCGTGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGA} \underline{\textbf{ATG}} \texttt{AAAGTTTCTATTCCAACTAAAGCC}$ TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAGCCTGC ATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGTCTC \mathtt{TGTG} AGACTGTTTCACAGAAGGATGTGTGTTTACCCAAGGCTACACATCAAAAAGAAATAGATAAAAT AAAT GAAAATTAGAAGAGTCTCCTGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTT $\mathtt{CTATT} \dot{\boldsymbol{\chi}} \mathtt{CAACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCA}$ TCTGCC\TCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGA ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAGAAGGTTGAAGAAAATTCTT AAAGAAATĠĢATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTATCAAAAATCTTGGATACAGT TCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAAC AAATGAAAAAQAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTA GAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGA GAAGAGAAAAAGCCGATATATTAAAT AAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGC ATAGGAAAGAGTTAGAACAACAACAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG AGTGTAGAAAGTAA TTGAATCAGGTT TCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAA TTGCATGTTGAAAAA GAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGG AAAAGGAAAATAAATA&TTTGAGGACATTAAAGATTTTAAAAGAAAGAATGCTGAACTTCAGATGACC CTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTTAAAGTTCTGAT TTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGACCATCATCAAATTGTGACATCAAGAAAA AGTCAAGAACCTGCTTTCCACATTGCAGSAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAG TAGTACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGC ${\tt CTAAAAATTAATCTCAATTATG} {\tt CAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC}$ AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGAT NATGTGAACAACACTGANCAGCAGGAGTCTCTAGATCAGAATTATTTCAACTACAAAGCAAAAA TATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAAAGCAAGATAACAATT GATNTTCATTNTCTTGAGAGGAAAA TGCNCATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNAT

MKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADEILPSESKQKDYE ESSWDSESLCETVSQKDVCLPKATHQKEIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQT FKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADQMFPSESKQKKVEENSWDSESLRETVSQKD VCVPKATHQKEMDKISGKLEDSTSLSKILDTVHSCERARELQKDHCEQRTGKMEQMKKKFCVLKKKLS EAKEIKSQLENQKVKWEQELCSVRLTLNQEEEKRRNADILNEKIREELGRIEEQHRKELEVKQQLEQA LRIQDIELKSVESNLNQVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKEILEAEIESHHPRLASAVQD HDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTDI.

SEQ ID NO. 2

,GAGTAACCCGATAA1\ATGCCGTTGTGCACGGCGACGAGAATTCCCAGATATAGCAGTAGCAGTGATCCCGGGCCT GTGGCTCGGGGCCGGGCTGCAGTTCGGACCGCCTCCCGCGACCCGCGGGGCCGGCTCGGAGACAGTTTCAGGCC GCATCTTTGCTGACCC&AGGGTGGGGCCGCGTGGCCGTGGAAACAGATCCTGAAGGAGCTAGACGAGTGCTAC agccaggagctgggcgacaagatccagatcgtgagccagatggtggagctggtggagaaccgcacgcggcag GTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGC GCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGCCCAACAGCAAGCGCTCACGGCGGCAGCGCAAC AACGAGAACCGTGAGAACGACCACGACCACGACCACGCGCGCCTCGGGCACACCCAAGGAGAAGAAG GACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCGGCTGCGACAACGACGAG TGCCCCATCGAGTGGTTCCACTTCTCGTGCGTGGGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAG TGCCGGGGGGAGAACGAGAGACCATGGACAAAGCCOTGGAGAAATCCAAAAAGAGAGGGCTTACAACAGGTAG TTTGTGGACAGGCGCCTGGTGTGAGGACAAAAT AAACCGTGTATTTATTACATTGCTGCCTTTGTTGAGGTG CAAGGAGTGTAAAATGTATATTTTAAAAGAATGTTAGAAAAGGAACCATTCCTTTCATAGGGATGGCAGTGATTC TGTTTGCCTTTTGTTTTCATTGGTAQACGTGTAACAAGAGAAGTGGTCTGTGGATCAGCATTTTAGAAACTACAAA $\verb|TTAAATGTGGAAGGAAAATATTTCATI\| A GCTTTTT | | A TTTTAATACAAGTAATATTATTACTTTATGAACAATTT$ TTTTTAATTGGCCATGTCGCCAAAAATACAGCCTAAAGTAAATGTGTTTCTTGCTGCCATGATGTATATCCATAT AACAATTCAGTAACAAAGGTTTAAAGTTTGAAGATTATTTTTTAAAAAAGGTTAAATTTTACATGACAG ATATTTTATCTATTGGCCTGTTCCCCAAATGGCCATATTAAAATGCTTG>ACACTTCTCTTAAGTGGTCTAGT CAAGGAACCTCAAGTCATGCTTTTGCTAT¢ACCAATCATAGTGTACCCATCTTTAATTTATATCAGGTGTATAAA TGTACATTTCCAAATGAACTTGCACTGTAATATTATAATTGGAAGTGCAGTCAGCAGTAGCTGTCGGAGCTAATG t TTGGCCAGTTTGTTCCTCTAGTAGTATTTT ${ t ACACCAGCAATTTAGACAAAGCCTTAAGCAAA ackslash au TTTGTATTATTGTTCTCACTTATTATTAATAATGAAGTAGAA$ GTTACTTAATTGCCAGCAAATAAATACGTGTCAAAAAAGAATCTGTATTCAGACCCCTGGGGTCAGGAAATTACT

gi|2183221|gb|AAB60879.1| p33ING1 (\$\mathcal{GO} ID NO:|\mathcal{Z}\)
MPLCTATRIPRYSSSSDPGPVARGRGCSSDRLPRPAGPARRQFQAASLLTRGWGRAWPWKQILKELDECY
ERFSRETDGAQKRRMLHCVQRALIRSQELGDEKIQIVSOMVELVENRTRQVDSHVELFEAQQELGDTVGN
SGKVGADRPNGDAVAQSDKPNSKRSRRQRNNENRENASSNHDHDDGASGTPKEKKAKTSKKKKRSKAKAE
REASPADLPIDPNEPTYCLCNQVSYGEMIGCDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMD
KALEKSKKERAYNR

D:	MPLCTATRIPRYSSS	15
A:	MLSPANGEQLHLVNYXEDYLDSIESLPFDLQRNVSLMREIDAKYQEILKELDECYERFSRETDGAQKRRMLHCVQ	75
B:	MLHCVQ	6
C:	\ MEILKELDECYERFSRETDGAQKRRMLHCVQ	31
D:	SDPGPVARGRGCSSDRLARPAGPARRQFQAASLLTRGWGRAWPWKQILKELDECYERFSRETDGAQKRRMLHCVQ	90
A:	RALIRSQELGDEKIQIVSQ M VELVENRTRQVDSHVELF X AQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	150
B:	RALIRSQELGDEKIQIVSQMVELVENRTRQVDSHVELFEAQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	156
C:	RALIRSQELGDEKIQIVSQM\LEVENRTRQVDSHVE\FEAQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	106
D:	ralirsqelgdekiqivsqmv\tivenrtrqvdshv\tilfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskrs	165
A:	RRQRNNENRENASSNHDHDDGA\$GTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	225
B:	RRQRNNENRENASSNHDHDDGASGTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	231
C:	RRORNNENRENASSNHDHDDGASGTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	161
D:	RRQRNNENRENASSNHDHDDGASG\PKEKKAKT\$KKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	240
A:	CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMDKALEKSKKERAYNR.	279

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210

235

294

A = SEQ ID NO. 5 B = SEQ ID NO. 6 C = SEQ ID NO. 7 D = SEQ ID NO. 17

CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKIMDKAŁEKSKKERAYNR.

CDNDECPIEWFHFSCVGLNHKPKGKWXCPKCRGENEKTMDKALEKSKKERAYNR.

CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMDKALEKSKKERAYNR.